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Sequence Listing was accepted.
If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).
Reviewer: Keisha Douglas
Timestamp: [year=2009; month=2; day=17; hr=17; min=11; sec=16; ms=383;]
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Validated By CRFValidator v 1.0.3

Application No: 10599313 Version No: 2.0

Input Set:

Output Set:

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Finished: 2009-01-28 19:40:38.517
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 652 ms
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Total Errors: 0
No. of SeqIDs Defined: 35
Actual SeqID Count: 35

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W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)

Input Set:

Output Set:

Started: 2009-01-28 19:40:36.865
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Error code	Error Description

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SEQUENCE LISTING

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HWANG, Dong Soo

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<130> 20010-06USA

<140> 10599313
<141> 2009-01-28

<150> US 60/556,805
<151> 2004-03-26

<150> PCT/KR2005/000888
<151> 2005-03-25

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1 5 10 15

Tyr His Ser Gly Gly Ser Tyr His Gly Ser Gly Tyr His Gly Gly Tyr
20 25 30

Lys Gly Lys Tyr Tyr Gly Lys Ala Lys Lys Tyr Tyr Tyr Lys Tyr Lys
35 40 45

Asn Ser Gly Lys Tyr Lys Tyr Leu Lys Lys Ala Arg Lys Tyr His Arg

50 55 60

Lys Gly Tyr Lys Lys Tyr Tyr Gly Gly Gly Ser Ser
65 70 75

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<213> Artificial Sequence

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1 5 10 15

Pro Thr Tyr Lys Ala Lys Pro Ser Tyr Pro Pro Thr Tyr Lys Ala Lys
20 25 30

Pro Ser Tyr Pro Pro Thr Tyr Lys Ala Lys Pro Ser Tyr Pro Pro Thr
35 40 45

Tyr Lys Ala Lys Pro Ser Tyr Pro Pro Thr Tyr Lys
50 55 60

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<220>
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1 5 10 15

Pro Thr Tyr Lys Ala Lys Pro Ser Tyr Pro Pro Thr Tyr Lys Ala Lys
20 25 30

Pro Ser Tyr Pro Pro Thr Tyr Lys Ala Lys Pro Ser Tyr Pro Pro Thr
35 40 45

Tyr Lys Ala Lys Pro Ser Tyr Pro Pro Thr Tyr Lys Ser Ser Glu Glu
50 55 60

Tyr Lys Gly Gly Tyr Tyr Pro Gly Asn Ser Asn His Tyr His Ser Gly
65 70 75 80

Gly Ser Tyr His Gly Ser Gly Tyr His Gly Gly Tyr Lys Gly Lys Tyr
85 90 95

Tyr Gly Lys Ala Lys Lys Tyr Tyr Tyr Lys Tyr Lys Asn Ser Gly Lys
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Lys Tyr Tyr Gly Gly Ser Ser Glu Phe
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aagaaatact attataaata taaaaacagc ggaaaataca agtatctaaa gaaagctaga 180

aaataccata gaaagggtta caagaagtat tatggaggta gcagtgaatt cgctaaaccg 240

tcttacccgc cgacctacaa agcaaaaccc tcgtacccac cgacttataa ggctaaacct 300

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<213> Artificial Sequence

<220>
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Tyr His Ser Gly Gly Ser Tyr His Gly Ser Gly Tyr His Gly Gly Tyr
20 25 30

Lys Gly Lys Tyr Tyr Gly Lys Ala Lys Lys Tyr Tyr Tyr Lys Tyr Lys
35 40 45

Asn Ser Gly Lys Tyr Lys Tyr Leu Lys Lys Ala Arg Lys Tyr His Arg
50 55 60

Lys Gly Tyr Lys Lys Tyr Tyr Gly Gly Ser Ser Glu Phe Ala Lys Pro
65 70 75 80

Ser Tyr Pro Pro Thr Tyr Lys Ala Lys Pro Ser Tyr Pro Pro Thr Tyr
85 90 95

Lys Ala Lys Pro Ser Tyr Pro Pro Thr Tyr Lys Ala Lys Pro Ser Tyr
100 105 110

Pro Pro Thr Tyr Lys Ala Lys Pro Ser Tyr Pro Pro Thr Tyr Lys Ala
115 120 125

Lys Pro Ser Tyr Pro Pro Thr Tyr Lys
130 135

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gcaaaaccgt cctaccctcc gacctataag gctaaaccga gttacccccc gacttacaaa 180

agttctgaag aatacaaggg tggttattac ccaggcaatt cgaaccacta tcattcaggt 240

ggtagttatc acggatccgg ctaccatgga ggatataagg gaaagtatta cggaaaggca 300

aagaaatact attataaata taaaaacagc ggaaaataca agtatctaaa gaaagctaga 360

aaataccata gaaagggtta caagaagtat tatggaggta gcagtgaatt cgctaaaccg 420

tcttacccgc cgacctacaa agcaaaaccc tcgtacccac cgacttataa ggctaaacct 480

agctatccac ctacgtacaa agctaaaccg tcttacccgc cgacttacaa agcaaaaccg 540

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<220>
<223> Bioadhesive protein(mgfp-151)

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Pro Thr Tyr Lys Ala Lys Pro Ser Tyr Pro Pro Thr Tyr Lys Ala Lys
            20                  25                  30

Pro Ser Tyr Pro Pro Thr Tyr Lys Ala Lys Pro Ser Tyr Pro Pro Thr
        35                  40                  45

Tyr Lys Ala Lys Pro Ser Tyr Pro Pro Thr Tyr Lys Ser Ser Glu Glu
    50                  55                  60

Tyr Lys Gly Gly Tyr Tyr Pro Gly Asn Ser Asn His Tyr His Ser Gly
65                  70                  75                  80

Gly Ser Tyr His Gly Ser Gly Tyr His Gly Gly Tyr Lys Gly Lys Tyr
                85                  90                  95

Tyr Gly Lys Ala Lys Lys Tyr Tyr Tyr Lys Tyr Lys Asn Ser Gly Lys
            100                 105                 110

Tyr Lys Tyr Leu Lys Lys Ala Arg Lys Tyr His Arg Lys Gly Tyr Lys
        115                 120                 125

Lys Tyr Tyr Gly Gly Ser Ser Glu Phe Ala Lys Pro Ser Tyr Pro Pro
    130                 135                 140

Thr Tyr Lys Ala Lys Pro Ser Tyr Pro Pro Thr Tyr Lys Ala Lys Pro
145                 150                 155                 160

Ser Tyr Pro Pro Thr Tyr Lys Ala Lys Pro Ser Tyr Pro Pro Thr Tyr
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Pro Pro Thr Tyr Lys
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tgcagcagtt ctgaagaata caagggtggt tattacccag gcaattcgaa ccactatcat 180

tcaggtggta gttatcacgg atccggctac catggaggat ataagggaaa gtattacgga 240

aaggcaaaga aatactatta taaatataaa aacagcggaa aatacaagta tctaaagaaa 300

gctagaaaat accatagaaa gggttacaag aagtattat 339

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Gly Gly Gln Gln Met Gly Arg Thr Leu Tyr Asp Asp Asp Asp Lys Asp
20 25 30

Arg Trp Gly Ser Glu Leu Glu Ile Cys Ser Ser Ser Glu Glu Tyr Lys
35 40 45

Gly Gly Tyr Tyr Pro Gly Asn Ser Asn His Tyr His Ser Gly Gly Ser
50 55 60

Tyr His Gly Ser Gly Tyr His Gly Gly Tyr Lys Gly Lys Tyr Tyr Gly
65 70 75 80

Lys Ala Lys Lys Tyr Tyr Tyr Lys Tyr Lys Asn Ser Gly Lys Tyr Lys
85 90 95

Tyr Leu Lys Lys Ala Arg Lys Tyr His Arg Lys Gly Tyr Lys Lys Tyr
100 105 110

Tyr Gly Gly Ser Ser
115

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<211> 435
<212> DNA
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cctacgtaca aagctaaacc gtcttacccg ccgacttaca aagcaaaacc gtcctaccct 180

ccgacctata aggctaaacc gagttacccc ccgacttaca aaggctgcag ttctgaagaa 240

tacaagggtg gttattaccc aggcaattcg aaccactatc attcaggtgg tagttatcac 300

ggatccggct accatggagg atataaggga aagtattacg gaaaggcaaa gaaatactat 360

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<210> 18
<211> 151
<212> PRT
<213> Artificial Sequence

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<400> 18

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1 5 10 15

Pro Ser Tyr Pro Pro Thr Tyr Lys Ala Lys Pro Ser Tyr Pro Pro Thr
20 25 30

Tyr Lys Ala Lys Pro Ser Tyr Pro Pro Thr Tyr Lys Ala Lys Pro Ser
35 40 45

Tyr Pro Pro Thr Tyr Lys Ala Lys Pro Ser Tyr Pro Pro Thr Tyr Lys
50 55 60

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Ala Lys Pro Ser Tyr Pro Pro Thr Tyr Lys Gly Cys Ser Ser Glu Glu
65                  70                  75                  80

Tyr Lys Gly Gly Tyr Tyr Pro Gly Asn Ser Asn His Tyr His Ser Gly
                85                  90                  95

Gly Ser Tyr His Gly Ser Gly Tyr His Gly Gly Tyr Lys Gly Lys Tyr
            100                 105                 110

Tyr Gly Lys Ala Lys Lys Tyr Tyr Tyr Lys Tyr Lys Asn Ser Gly Lys
        115                 120                 125

Tyr Lys Tyr Leu Lys Lys Ala Arg Lys Tyr His Arg Lys Gly Tyr Lys
    130                 135                 140

Lys Tyr Tyr Gly Gly Ser Ser
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tcaggtggta gttatcacgg atccggctac catggaggat ataagggaaa gtattacgga 240

aaggcaaaga aatactatta taaatataaa aacagcggaa aatacaagta tctaaagaaa 300

gctagaaaat accatagaaa gggttacaag aagtattatg gaggtagcag tgaattcgct 360

aaaccgtctt acccgccgac ctacaaagca aaaccctcgt acccaccgac ttataaggct 420

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20 25 30

Arg Trp Gly Ser Glu Leu Glu Ile Cys Ser Ser Ser Glu Glu Tyr Lys
35 40 45

Gly Gly Tyr Tyr Pro Gly Asn Ser Asn His Tyr His Ser Gly Gly Ser
50 55 60

Tyr His Gly Ser Gly Tyr His Gly Gly Tyr Lys Gly Lys Tyr Tyr Gly
65 70 75 80

Lys Ala Lys Lys Tyr Tyr Tyr Lys Tyr Lys Asn Ser Gly Lys Tyr Lys
85 90 95

Tyr Leu Lys Lys Ala Arg Lys Tyr His Arg Lys Gly Tyr Lys Lys Tyr
100 105 110

Tyr Gly Gly Ser Ser Glu Phe Ala Lys Pro Ser Tyr Pro Pro Thr Tyr
115 120 125

Lys Ala Lys Pro Ser Tyr Pro Pro Thr Tyr Lys Ala Lys Pro Ser Tyr
130 135 140

Pro Pro Thr Tyr Lys Ala Lys Pro Ser Tyr Pro Pro Thr Tyr Lys Ala
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Thr Tyr Lys

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cctacgtaca aagctaaacc gtcttacccg ccgacttaca aagcaaaacc gtcctaccct 180

ccgacctata aggctaaacc gagttacccc ccgacttaca aaggctgcag ttctgaagaa 240

tacaagggtg gttattaccc aggcaattcg aaccactatc attcaggtgg tagttatcac 300

ggatccggct accatggagg atataaggga aagtattacg gaaaggcaaa gaaatactat 360

tataaatata aaaacagcgg aaaatacaag tatctaaaga aagctagaaa ataccataga 420

aagggttaca agaagtatta tggaggtagc agtgaattcg ctaaaccgtc ttacccgccg 480

acctacaaag caaaaccctc gtacccaccg acttataagg ctaaacctag ctatccacct 540

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